



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) Nico Cerletti

(ii) TITLE OF INVENTION: New process for the production of
biologically active protein

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS

(A) ADDRESSEE: Novartis Patent Department
(B) STREET: 564 Morris Avenue
(C) CITY: Summit
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07901

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/776,444
(B) FILING DATE: 24-JAN-97

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP95/02719
(B) FILING DATE: 12-Jul-95
(A) APPLICATION NUMBER: EPO 94810439.3
(B) FILING DATE: 25-Jul-94

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 522-6940
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..336

(D) OTHER INFORMATION: /product= "human TGF-beta1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	48
1 5 10 15	
GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	96
20 25 30	
ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC CTC GGG CCC TGC Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys	144
35 40 45	
CCC TAC ATT TGG AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu	192
50 55 60	
TAC AAC CAG CAT AAC CCG GGC GCC TCG GCG CCG TGC TGC GTG CCG Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro	240
65 70 75 80	
CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC GTG GGC CGC AAG CCC Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro	288
85 90 95	
AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CGC TCC TGC AAG TGC AGC Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser	336
100 105 110	
TGA	339

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	

Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly	Pro	Cys
35	.						40					45			
Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu	Ala	Leu
50							55				60				
Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys	Val	Pro
65					70						75				80
Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg	Lys	Pro
							85				90				95
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys	Cys	Ser
								100			105				110

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: E. coli LC137/pPLMu.hTGF-beta2 (DSM5657)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION:/product= "human TGF-beta2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC 48
 Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys
 115 120 125

CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG 96
 Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp
 130 135 140

ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGT GCT GGA GCA TGC	144
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys	
145 150 155 160	

CCG TAT TTA TGG AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA 192
 Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu
 165 170 175

TAT AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC GTG TCC 240
 Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser
 180 185 190

CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC ATT GGC AAA ACA CCC	288
Gln Asp Leu Glu Pro Lèu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro	
195 . 200 205	
AAG ATT GAA CAG CTT TCT AAT ATG ATT GTA AAG TCT TGC AAA TGC AGC	336
Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
210 215 220	
TAA	339

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 -) MOLECULE TYPE: protein
 -) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys
 1 5 10 15

Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp
 20 25 30

Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys
 35 40 45

Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu
 50 55 60

Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser
 65 70 75 80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro
 85 90 95

Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - vii) IMMEDIATE SOURCE:
 - (B) CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION:1..336
(D) OTHER INFORMATION:/product= "human TGF-beta3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	115	120	125	48
GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG GAT CTG GGC TGG AAG TGG Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	130	135	140	96
GTC CAT GAA CCT AAG GGC TAC TAT GCC AAC TTC TGC TCA GGC CCT TGC Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys	145	150	155	144
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	165	170	175	192
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	180	185	190	240
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	195	200	205	288
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	210	215	220	336
TGA				339

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys
1					5					10				15	
Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp
										20			25		30
Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys
										35			40		45
Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu
										50			55		60

Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro
65					70						75			80	
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg	Thr	Pro
					85				90				95		
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys	Cys	Ser
					100				105				110		

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "recombinant hybrid DNA of TGF-beta1 and TGF-beta3 DNA"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..132
- (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta1"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta named TGF-beta1-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCC	CTG	GAC	ACC	AAC	TAT	TGC	TTC	AGC	TCC	ACG	GAG	AAG	AAC	TGC	TGC	48
Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	
1					5					10			15			

GTG	CGG	CAG	CTG	TAC	ATT	GAC	TTC	CGC	AAG	GAC	CTC	GGC	TGG	AAG	TGG	96
Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	
					20				25				30			

ATC	CAC	GAG	CCC	AAG	GGC	TAC	CAT	GCC	AAC	TTC	TGC	TCA	GGC	CCT	TGC	144
Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	
								35	40				45			

CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192		
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu			
50	55	60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240		
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro			
65	70	75	80
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288		
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro			
85	90	95	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336		
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser			
100	105	110	

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys			
1	5	10	15
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp			
20	25	30	
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys			
35	40	45	
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu			
50	55	60	
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro			
65	70	75	80
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro			
85	90	95	
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser			
100	105	110	

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "recombinant hybrid DNA"

coding for hybrid TGF-beta2-3"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3.

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..132
(D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta2"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:133..336
(D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..336
(D) OTHER INFORMATION:/product= "hybrid TGF-beta2-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC	48
Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys	
1 5 10 15	
CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG	96
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp	
20 25 30	
ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
65 70 75 80	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
85 90 95	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Ala	Leu	Asp	Ala	Ala	Tyr	Cys	Phe	Arg	Asn	Val	Gln	Asp	Asn	Cys	Cys
1					5			10						15	
Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp	Lys	Trp
					20			25					30		
Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys
					35			40				45			
Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu
					50			55			60				
Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro
					65			70			75		80		
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg	Thr	Pro
					85				90			95			
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys	Cys	Ser
					100				105			110			

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "recombinant hybrid DNA coding for hybrid TGF-beta3-2"

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..132
 - (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta3"

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:133..336
 - (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta2"

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "hybrid TGF-beta3-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	48
1 5 10 15	
GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG GAT CTG GGC TGG AAG TGG Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	96
20 25 30	
GTC CAT GAA CCT AAG GGC TAC TAT GCC AAC TTC TGT GCT GGA GCA TGC Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ala Gly Ala Cys	144
35 40 45	
CCG TAT TTA TGG AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	192
50 55 60	
TAT AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC GTG TCC Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	240
65 70 75 80	
CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC ATT GGC AAA ACA CCC Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro	288
85 90 95	
AAG ATT GAA CAG CTT TCT AAT ATG ATT GTA AAG TCT TGC AAA TGC AGC Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	336
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
1 5 10 15	
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
20 25 30	
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ala Gly Ala Cys	
35 40 45	
Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	
50 55 60	
Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	
65 70 75 80	

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro
85 " 90 95

Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGGAATTCC GG

12